

Figure 1 (SEQ ID NO:1)

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1 ATGAAGAAAC ATCTTAAAC AGTTGCCTTG ACCCTCACTA CAGTATCGGT AGTCACCCAC
61 AATCAGGAAG TTTTCTAGTTT AGTCAAAGAG CCAATTCTTA AACAAACTCA AGCTTCTTCA
121 TCGATTTCTG GCGCTGACTA CGCAGAAAGT AGCGGTAAAA GCAAGTTAAA GATTAATGAA
181 ACTTCTGGCC CTGTTGATGA TACAGTCACT GACTTATTTT CGGATAAACG TACTACTCCT
241 GAAAAAATAA AAGATCTTCT TGCTAAAGGT CCGAGAGAAC AAGAGTTAAA GGCAGTAACA
301 GAGAATACAG AATCAGAAAA GCAGATCACT TCTGGATCTC AACTAGAACA ATCAAAAGAG
361 TCTCTTTCTT TAAATAAAAC AGTGCCATCA ACGTCTAATT GGGAGATTTG TGATTTTATT
421 ACTAAGGGGA ATACCCCTGT TGGTCTTTCA AAATCAGGTG TTGAAAAGTT ATCTCAAAC
481 GATCATCTCG TATTGCC TAGCAGCA GATGGAAC TC AATTGATACA AGTAGCTAGT
541 TTTGCTTTTA CTCCAGATAA AAAGACGGCA ATTGCAGAAT ATACCAGTAG GGCTGGAGAA
601 AATGGGGAAA TAAGCCAACT AGATGTGGAT GGAAAAGAAA TTATTAACGA AGGTGAGGTT
661 TTTAATTCTT ATCTACTAAA GAAGGTAACA ATCCCAACTG GTTATAAACA TATTGGTCAA
721 GATGCTTTTG TGGACAATAA GAATATTGCT GAGGTTAATC TTCCTGAAAG CCTCGAGACT
781 ATTTCTGACT ATGCTTTTGC TCACCTAGCT TTGAAACAGA TCGATTTGCC AGATAATTTA
841 AAAGCGATTG GAGAATTAGC TTTTCTTGT AATCAAATTA CAGGTAAACT TTCTTTGCCA
901 CGTCAGTTAA TGCGATTAGC AGAACGTGCT TTTAAATCAA ACCATATCAG AACAAATTGAG
961 TTTAGAGGAA ATAGTCTAAA AGTGATAGGG GAAGCTAGTT TTCAAGATAA TGATCTGAGT
1021 CAACTAATGC TACCTGACGG TCTTGAAAAA ATAGAATCAG AAGCTTTTAC AGGAAATCCA
1081 GGAGATGATC ACTACAATAA CCGTGTGTGT TTGTGGACAA AATCTGGAAA AAATCCTTCT
1141 GGTCTTGCTA CTGAAAATAC CTATGTTAAT CCTGATAAGT CACTATGCCA GGAAAAGTCCT
1201 GAGATTGATT ATACTAAATG GTTAGAGGAA GATTTTACCT ATCAAAAAAA TAGTGTTACA
1261 GGTTTTTCAA ATAAAGGCTT AAAAAAGTA AAACGTAATA AAAACTTAGA AATTCACAAA
1321 CAGCACAATG GTGTTACTAT TACTGAAATT GGTGATAATG CTTTTTCGCA TGTGATTTT
1381 CAAAATAAAA CTTTACGTAA ATATGATTTG GAAGAAGTAA AGCTTCCCTC AACTATTCGG
1441 AAAATAGGTG CTTTTGCTTT TCAATCTAAT AACTTGAAAT CTTTTGAAGC AAGTGACGAT
1501 TTAGAAGAGA TTAAAGAGGG AGCCTTTATG AATAATCGTA TTGAAACCTT GGAATTAATA
1561 GATAAATTAG TTACTATTGG TGATGCGGCT TTCCATATTA ATCATATTTA TGCCATTGTT
1621 CTTCCAGAAT CTGTACAAGA AATAGGGCGT TCAGCATTTT GCAGAAATGG TGCAATAAT
1681 CTTATTTTGA TGGGAAGTAA GGTAAAGACC TTAGGTGAGA TGGCATTTT ATCAAAATAG
1741 CTTGAACATC TGGATCTTTC TGAGCAAAAA CAGTTAACAG AGATTCTCTG TCAAGCCTTT
1801 TCAGACAATG CCTTGAAAGA AGTATTATTA CCAGCATCAC TGAAAACGAT TCGAGAAGAA
1861 GCCTTCAAAA AGAATCATTT AAAACAACTG GAAGTGGCAT CTGCCTTGTC CCATATTGCT
1921 TTTAATGCTT TAGATGATAA TGATGGTGAT GAACAATTTG ATAATAAAGT GGTGTGTTAA
1981 ACGCATCATA ATTCCTACGC ACTAGCAGAT GGTGAGCATT TTATCGTTGA TCCAGATAAG
2041 TTATCTTCTA CAATAGTAGA CCTTGAAAAG ATTTTAAAC TAATCGAAGG TTTAGATTAT
2101 TCTACATTAC GTCAGACTAC TCAAACTCAG TTTAGAGACA TGACTACTGC AGGTAAAGCG
2161 TTGTTGTCAA AATCTAACCT CCGACAAGGA GAAAAACAAA AATTCCTTCA AGAAGCACAA
2221 TTTTTCCTTG GCCGCTTGA TTTGGATAAA GCCATAGCTA AAGCTGAGAA GGCTTTAGTG
2281 ACCAAGAAGG CAACAAAGAA TGGTCAGTTG CTTGAAAGAA GTATTAACAA AGCGGTATTA
2341 GCTTATAATA ATAGCGCTAT TAAAAAGCT AATGTTAAGC GCTTGAAAA AGAGTTAGAC
2401 TTGCTAACAG GATTAGTTGA GGGAAAAGGA CCATTAGCGC AAGCTACAAT GGTACAAGGA
2461 GTTTATTTAT TAAAGACGCC TTTGCCATTG CCAGAATATT ATATCGGATT GAACGTTTAT
2521 TTTGACAAGT CTGGAAAATT GATTTATGCA CTTGATATGA GTGATACTAT TGGCGAGGGA
2581 CAAAAAGACG CTTATGGTAA TCCTATATTA AATGTTGACG AGGATAATGA AGGTATCAT
2641 GCCTTGGCAG TTGCCACTTT AGCTGATTAT GAGGGGCTCG ACATCAAAAC AATTTTAAAT
2701 AGTAAGCTTA GTCAATTAAC ATCTATTCGT CAGGTACCGA CTGCAGCCTA TCATAGAGCC
2761 GGTATTTTCC AAGCTATCCA AAATGCAGCG GCAGAAGCAG AGCAGTTATT GCCTAAACCA
2821 GGTACGCACT CTGAGAAGTC AAGCTCAAGT GAATCTGCTA ACTCTAAAGA TAGAGGATTG
2881 CAATCAAACC CAAAAACGAA TAGAGGACGA CACTCTGCAA TATTGCCTAG GACAGGGTCA
2941 AAAGGCAGCT TTGTCTATGG AATCTTAGGT TACACTAGCG TTGCTTTACT GTCACATAA
3001 ACTGCTATAA AAAAGAAAAA ATATTAA

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Figure 2 (SEQ ID NO:2)

1 MKKHLKTVAL TLTTVSUVTH NOEVFSLVKE PILKQTQASS SISGADYAES SGKSKLKINE
61 TSGPVDDTVT DLFSDKRTTP EKIKNLAKG PREQELKAVT ENTESEKQIT SGSQLEQSKE
121 SLSLNKTVPS TSNWEICDFI TKGNTLVGLS KSGVEKLSQT DHLVLPSQAA DGTQLIQVAS
181 FAFTPDKKTA IAEYTSRAGE NGEISQLDVD GKEIINEGEV FNSYLLKKVT IPTGYKHIGQ
241 DAFVDNKNIA EVNLPESLET ISDYAFAHLA LKQIDLDPNL KAIGELAFFD NQITGKLSLP
301 RQLMRLAERA FKSNIHKTIE FRGNSLKVIG EASFQDNDLS QLMPLDGLEK IESEFTGNP
361 GDDHYNNRVV LWTGSGKNPS GLATENTYVN PDKSLWQESP EIDYTKWLEE DFTYQKNSVT
421 GFSNKGLOKV KRNKNLEIPK QHNGVTITEI GDNAFRNVDF QNKTLRKYDL EEVKLPSTIR
481 KIGAFAFQSN NLKSFEASDD LEEIKEGAFM NNRIETLELK DKLVTIGDAA FHINHIYAIV
541 LPESVQEIGR SAFRQNGANN LIFMGSKVKT LGEMAFLSNR LEHLDLSEQK QLTEIPVQAF
601 SDNALKEVLL PASLKTIREE AFKKNHLKQL EVASALSHIA FNALDDNDGD EQFDNKVVVK
661 THHNSYALAD GEHFIVDPDK LSSTIVDLEK ILKLIEGLDY STLRQTTQTQ FRDMTTAGKA
721 LLSKSNLROG EKQKFLQEAQ FFLGRVDLDK AIAKA EKALV TKKATKNGQL LERSINKAVL
781 AYNNSAIKKA NVKRLEKELD LLTGLVEGKG PLAQATMVQG VYLLKTPLPL PEYYIGLNVY
841 FDKSGKLIYA LDMSDTIGEG QKDAYGNPIL NVDEDNEGYH ALAVATLADY EGLDIKTILN
901 SKLSQLTSIR QVPTAAYHRA GIFQAIQNAA AEAEQLLPKP GTHSEKSSSS ESANSKDRGL
961 QSNPKTNRGR HSAILPRTGS KGSFVYGILG YTSVALLSLI TAIKKKKY*

Figure 3

Clustal W(1.4) multiple sequence alignment

7 Sequences Aligned.. Alignment Score = 118839
 Gaps Inserted = 0 Conserved Identities = 936

Pairwise Alignment Mode: Fast
 Pairwise Alignment Parameters:
 ktrp = 1 Gap Penalty = 3 Top Diagonals = 5 Window Size = 5

Multiple Alignment Parameters:
 Open Gap Penalty = 10.0 Extend Gap Penalty = 0.1
 Delay Divergent = 40% Gap Distance = 8
 Similarity Matrix: blosum

Processing time: 12.9 seconds

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Spy74_M3      1      DYAES      5
Spy70_M5      1      LVKEPILKQTQASSSISGADYAES 24
Spy69_M6      1      KQTQASSSISGADYAES 17
Spy68_M2      1      LVKEPILKQTQASSSISGADYAES 24
Spy60_M1      1      LVKEPILKQTQASSSISGADYAES 24
12357_M18     1      VKEPILKQTQASSSISGADYAES 23
700294_M1     1 MKKHLKTVALTLTTSVVTHNQEVFSLVKEPILKQTQASSSISGADYAES 50
               *****

Spy74_M3      6 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 55
Spy70_M5     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
Spy69_M6     18 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 67
Spy68_M2     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
Spy60_M1     25 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 74
12357_M18    24 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 73
700294_M1    51 SGKSKLKINETSGPVDDTVTDLFSDKRTTPEKIKDNLAKGPREQELKAVT 100
               *****

Spy74_M3     56 ENTESEKQITSGSQLEQSKESLSLNKRVPTSTSNWEICDFITKGNTLVGLS 105
Spy70_M5     75 ENTESEKQINSGSQLEQSKESLSLNKRVPTSTSNWEICDFITKGNTLVGLS 124
Spy69_M6     68 ENTESEKQINSGSQLEQSKESLSLNKRVPTSTSNWEICDFITKGNTLVGLS 117
Spy68_M2     75 ENTESEKQITSGSQLEQSKESLSLNKTVPTSTSNWEICDFITKGNTLVGLS 124
Spy60_M1     75 ENTESEKQITSGSQLEQSKESLSLNKTVPTSTSNWEICDFITKGNTLVGLS 124
12357_M18    74 ENTESEKQINSGSQLEQSKESLSLNKRVPTSTSNWEICDFITKGNTLVGLS 123
700294_M1    101 ENTESEKQITSGSQLEQSKESLSLNKTVPTSTSNWEICDFITKGNTLVGLS 150
               *****

Spy74_M3     106 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 155
Spy70_M5     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
Spy69_M6     118 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 167
Spy68_M2     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
Spy60_M1     125 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 174
12357_M18    124 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 173
700294_M1    151 KSGVEKLSQTDHLVLPQAADGTQLIQVASFAFTPDKKTAIAEYTSRAGE 200
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Spy74_M3	156	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	205
Spy70_M5	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy69_M6	168	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	217
Spy68_M2	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
Spy60_M1	175	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	224
12357_M18	174	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	223
700294_M1	201	NGEISQLDVGKEIINEGEVFNSYLLKKVTIPTGYKHIGQDAFVDNKNIA	250

Spy74_M3	206	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	255
Spy70_M5	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy69_M6	218	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	267
Spy68_M2	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
Spy60_M1	225	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	274
12357_M18	224	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	273
700294_M1	251	EVNLPESLETISDYAFAHLALKQIDLPDNLKAIGELAFFDNQITGKLSLP	300

Spy74_M3	256	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	305
Spy70_M5	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy69_M6	268	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	317
Spy68_M2	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
Spy60_M1	275	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	324
12357_M18	274	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	323
700294_M1	301	RQLMRLAERAFKSNHIKTIEFRGNSLKVIGEASFQDNDLSQLMLPDGLEK	350

Spy74_M3	306	IESEAPTGNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	355
Spy70_M5	325	IESEAPTGNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy69_M6	318	IESEAPTGNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	367
Spy68_M2	325	IESEAPTGNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	374
Spy60_M1	325	IESEAPTGNPGDDHYNRRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	374
12357_M18	324	IESEAPTGNPGDDHYNRRVVLWTKSGKNPYGLATENTYVNPDKSLWQESP	373
700294_M1	351	IESEAPTGNPGDDHYNRRVVLWTKSGKNPSGLATENTYVNPDKSLWQESP	400

Spy74_M3	356	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	405
Spy70_M5	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	424
Spy69_M6	368	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	417
Spy68_M2	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	424
Spy60_M1	375	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	424
12357_M18	374	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	423
700294_M1	401	EIDYTKWLEEDFTYQKNSVTGFSSKGLQKVKNKNLEIPKQHNGVTITEI	450

Spy74_M3	406	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	455
Spy70_M5	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	474
Spy69_M6	418	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	467
Spy68_M2	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	474
Spy60_M1	425	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	474
12357_M18	424	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	473
700294_M1	451	GDNAFRNVDFQNKTLRKYDLEEVKLPSTIRKIGAFQSNMNLKSFEASDD	500

Spy74_M3	456	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	505
Spy70_M5	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy69_M6	468	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	517
Spy68_M2	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
Spy60_M1	475	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	524
12357_M18	474	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	523
700294_M1	501	LEEIKEGAFMNNRIETLELKDKLVTIGDAAFHINHIYAIVLPESVQEIGR	550

Spy74_M3	506	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	555
Spy70_M5	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy69_M6	518	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	567
Spy68_M2	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
Spy60_M1	525	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	574
12357_M18	524	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	573
700294_M1	551	SAFRQNGANNLIFMGSKVKTIGEMAFLSNRLEHLDLSEQKQLTEIPVQAF	600

Spy74_M3	556	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	605
Spy70_M5	575	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	624
Spy69_M6	568	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	617
Spy68_M2	575	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	624
Spy60_M1	575	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	624
12357_M18	574	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	623
700294_M1	601	SDNALKEVLLPASLKTIREEAFKQNHKQLEVASALSHTAFNALDDNDGD	650

Spy74_M3	606	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	655
Spy70_M5	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
Spy69_M6	618	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	667
Spy68_M2	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
Spy60_M1	625	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	674
12357_M18	624	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	673
700294_M1	651	EQFDNKVVVKTHHNSYALADGEHFIVDPDKLSSTMVDLEKILKLEGLDY	700

Spy74_M3	656	STLRQTTQTQFRDMTTAGKALLSKSKLRQGEKQKFLQEAQFFLGRVDLDK	705
Spy70_M5	675	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	724
Spy69_M6	668	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	717
Spy68_M2	675	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	724
Spy60_M1	675	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	724
12357_M18	674	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	723
700294_M1	701	STLRQTTQTQFRDMTTAGKALLSKSKNLROGEKQKFLQEAQFFLGRVDLDK	750

Spy74_M3	706	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	755
Spy70_M5	725	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy69_M6	718	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	767
Spy68_M2	725	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
Spy60_M1	725	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	774
12357_M18	724	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	773
700294_M1	751	AIKAEKALVTKKATKNGQLLGRSINKAVLAYNNSAIKKANVKRLEKELD	800

Spy74_M3	756	LLTGLV2GKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	805
Spy70_M5	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy69_M6	768	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	817
Spy68_M2	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
Spy60_M1	775	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	824
12357_M18	774	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	823
700294_M1	801	LLTGLVEGKGPLAQATMVQGVYLLKTPLPLPEYYIGLNVYFDKSGKLIYA	850

Spy74_M3	806	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	855
Spy70_M5	825	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	874
Spy69_M6	818	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	867
Spy68_M2	825	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	874
Spy60_M1	825	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	874
12357_M18	824	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	873
700294_M1	851	LDMSDTIGEGQKDAYGNPILNVEDNEGYHALAVATLADYEGLDIKTILN	900

Spy74_M3	856	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	905
Spy70_M5	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKAGTHSEKSSSS	924
Spy69_M6	868	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	917
Spy68_M2	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	924
Spy60_M1	875	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	924
12357_M18	874	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	923
700294_M1	901	SKLSQLTSIRQVPTAAYHRAGIFQAIQNAAAEAEQLLPKPGTHSEKSSSS	950

Spy74_M3	906	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	951
Spy70_M5	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	970
Spy69_M6	918	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	963
Spy68_M2	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	971
Spy60_M1	925	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	971
12357_M18	924	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVAL	969
700294_M1	951	ESANSKDRGLQSNPKTNRGRHSAILPRTGSKGSFVYGILGYTSVALSLI	1000

Spy74_M3	952	951
Spy70_M5	971	970
Spy69_M6	964	963
Spy68_M2	972	971
Spy60_M1	972	971
12357_M18	970	969
700294_M1	1001	TAIKKKKY 1008